

Figure No. 1

1 A	TGGCCGCTCGCGGCGTGCTGAACGCGCCGCGGGCGCCGGAGACGGTCGGCGAGGACAGCGT
1 M	SetAlaAlaArgGlyGlyAlaGluArgAlaAlaGlyAlaGlyAspGlyArgArgGlyGlnArg
64 C	GTCATCTACGACCGGGACGTGTTCTCGCTGCTCTACGCGGTCCTGCAGCGCCTGGCGCCGGC
22 PA	rgHisLeuArgProGlyArgValleuAlaAlaLeuArgGlyProAlaAlaProGlyAlaGly
127	GGGCGCGCGCGCTAGCCGCTGCCCTGCTATGGGCGACGTGGGCCCCTGCTGCTGCCGGCG
43 <b>•</b> G	SlyAlaArgAlaAlaLeuAlaAlaLeuLeuTrpAlaThrTrpAlaLeuLeuLeuAlaAla
190	CCGCCGCGGGGCGACCGACAACGCCCCCGGCCCCCGCCGAAGAGGCCGCGAGCCCG
64 F	roAlaAlaGlyArgProAlaThrThrProProAlaProProGluGluAlaAlaSerPro
	CGCCCCCGCGAGCCCCAGCCCCCCGGCCCCGACGACGACG
85 <b>≯</b> A	laProProAlaSerProSerProProGlyProAspGlyAspAspAlaAlaSerProAspAsn
	AGCACAGACGTGCGCGCGCGCTCCGGCTCGCGCAGGCGGGAAAACTCGCGCTTCTTC
106 - 8	SerThrAspValArgAlaAlaLeuArgLeuAlaGlnAlaAlaGlyGluAsnSerArgPhePhe
	TGTGCCCGCCCCCCGGGCGCCACGGTGGTCCGGCTCGCGCCGCGCGCG
127 <b>&gt;</b> V	/alCysProProProSerGlyAlaThrValValArgLeuAlaProAlaArgProCysProGlu
	PACGGGCTCGGGCGGAACTACACGGAGGGCATCGGCGTCATTTACAAGGAGAACATCGCGCCG
14871	lyrGlyLeuGlyArgAsmTyrThrGluGlyTleGlyVallleTyrLysGluAsmIleAlaPro
	TACACGTTCAAGGCCTACATTTACAAAAACGTGATCGTGACCACGACCTGGGCGGGC
103.1	TyrThrPheLysAlaTyrIleTyrLysAsnValIleValThrThrThrTrpAlaGlySerThr
	PACGCGGCCATTACAAACCAGTACACGGACCGCGTGCCCGTGGGCATGGGCGAGATCACGGAC
190 • 1	TyrAlaAlaIleThrAsnGlnTyrThrAspArgValProValGlyMetGlyGluIleThrAsp
	TGGTGGACAAGAAGTGGCGCTGCCTTTCGAAAGCCGAGTACCTGCGCAGCGGGCGCAAGGTG
211 <b>•</b> I	euValAsplyslysTrpArgCysleuSerlysAlaGluTyrleuArgSerGlyArgLysVal
	TGGCCTTTGACCGCGACGACGCCCTGGGAGGCGCCGCTGAAGCCTGCGCGCTGAGCGCG
232 • V	/alalaPheAspArgAspAspAspProTrpGluAlaProLeuLysProAlaArgLeuSerAla
	CCGGGGTGCGGGCTGGCACACGACGACGATGTGTACACGGCGCTGGGCTCGGCGGGGCTC
253▶₽	ProGlyValArgGlyTrpHisThrThrAspAspValTyrThrAlaLeuGlySerAlaGlyLeu
	TACCGCACGGGCACCTCTGTGAACTGCATCGTGGAAGAAGTGGAGGCGCGCTCGGTGTACCCG
274*1	TyrArgThrGlyThrSerValAsnCysIleValGluGluValGluAlaArgSerValTyrPro
	TACGACTCGTTCGCGCTCTCGACCGGGGACATTATCTACATGTCGCCCTTTTACGGGCTGCGC
295 <b>*1</b>	TyrAspSerPheAlaLeuSerThrGlyAspIleIleTyrMetSerProPheTyrGlyLeuArg
	GAGGGCGCGCACCGCGAGCACCAGGCTACTCGCCGGAGCGCTTCCAGCAGATCGAGGGCTA
316 • (	GluGlyAlaHisArgGluHisThrArgLeuLeuAlaGlyAlaLeuProAlaAspArgGlyLeu
	CTACAAGCGCGACATGGCCACGGGCCGGCGCCTCAAGGAGCCGGTCTCGCGGAACTTTTTGCG
337▶1	LeuGlnAlaArgHisGlyHisGlyProAlaProGlnGlyAlaGlyLeuAlaGluLeuPheAla
_	TACACAGCACGTGACGGTAGCCTGGGACTGGGTGCCCAAGCGCAAAAACGTGTGCTCGCTGGC
358▶1	TyrThrAlaArgAspGlySerLeuGlyLeuGlyAlaGlnAlaGlnLysAroValLeuAlaGly

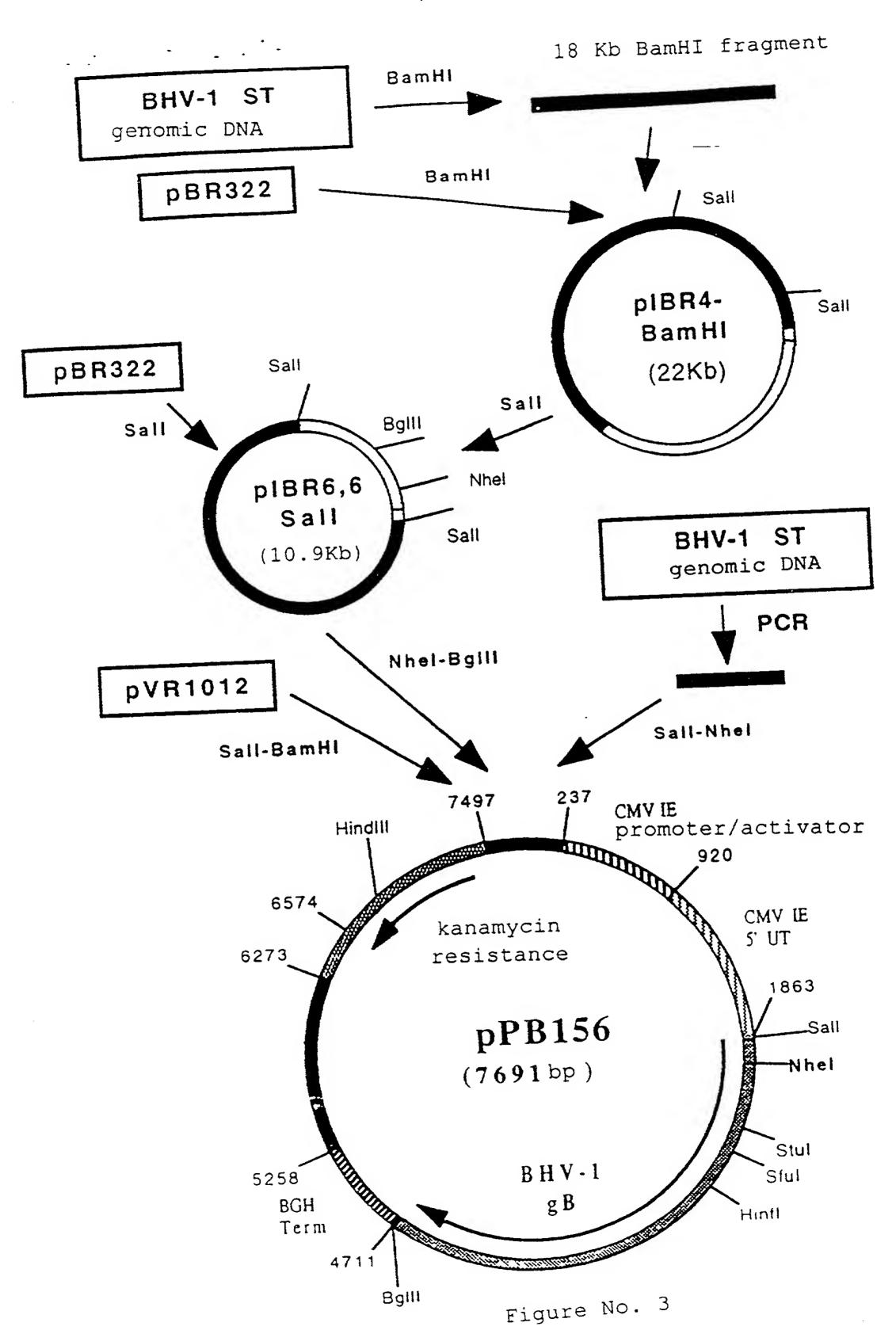
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1135 CAAGTGGCGCGAGGCGAAATGCTGCGAGACGAGAGCCGCGGGAACTTCCGCTTCACGGC
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400 ProleuAlaleuGlyAspleuCysGluArgGlnProHisleuArgValAlaGluCysAlaAla
1261 GAGCGACTGCGTGATCGAAGAGGCCGAGGCCGCGGTCGAGCGCGTCTACCGCGAGCGCTACAA
421 GluargleuargaspargargGlyargGlyargGlyargAlaargleuProargalaleuGln
1324 CGGCACGCACGTGCTGCGGCAGCTTGGAGACGTACCTGGCGCGCGC
442 ArgHisAlaArgAlaValGlyGlnLeuGlyAspValProGlyAlaArgArgLeuCysArgGly
1387 CTTCCGGCGATGCTCAGCAACGAGCTGGCCAAGCTGTACCTGCAGGAGCTGGCGCGCTCGAAC
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1513 GCCGCGCCGTCTGCGCCCGGCGGCGCCGGCGGCGCCGGCGG
505 AlaAlaProSerAlaProGlyGlyProGlyAlaAlaAsnGlyProAlaGlyAspGlyAspAla
1576 GGCGGGGGGGTGACTACCGTGAGCTCGGCCGAGTTTGCGGCGCGCTGCAGTTCACCTACGACCAC
526 GlyGlyArgValThrThrValSerSerAlaGluPheAlaAlaLeuGlnPheThrTyrAspHis
1639 ATCCAGGACCACGTGAACACCATGTTCAGCCGCCTGGCCACGTCCTGGTGCCTGCTGCAGAAC
547 IleGlnAspHisValAsmThrMetPheSerArgLeuAlaThrSerTrpCysLeuLeuGlnAsn
1702 AAGGAGCGCCCTGTGGGCCGAGGCGGCTAAGCTCAACCCCAGCGCGGCGCCAGCGCTGCG
568 LysGluargalaLeuTrpalaGlualaalaLysLeuAsnProSeralaalaalaSeralaala
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- 2269 ACGGACGCAATATGGCCATCATGCGAGGGCTCGCCAACTTCTTTCAGGGCCTGGGCGCCGTC 757 ThrAspGlyAsnMetAlaIleMetArgGlyLeuAlaAsnPhePheGlnGlyLeuGlyAlaVal
- 2332 GGGCAGGCGGTGGCACGGTGGTGCTGGGCGCGCGGGTGCCGCGCTCTCGACCGTGTCGGGC
- 778 GlyGlnAlaValGlyThrValValLeuGlyAlaAlaGlyAlaAlaLeuSerThrValSerGly
- 2395 ATCGCCTCGTTTATTGCGAACCCGTTCGGCGCGCTGGCCACGGGGCTGCTGGTGCTCGCCGGG
- 799 IleAlaSerPheIleAlaAsnProPheGlyAlaLeuAlaThrGlyLeuLeuValLeuAlaGly
- 2458 CTGGTGGCCGCTTTCCTGGCGTACCGGTACATTTCCCGCCTCCGCAGCAACCCCATGAAGGCG
- 820 LeuValAlaAlaPheLeuAlaTyrArgTyrIleSerArgLeuArgSerAsnProMetLysAla
- 2521 CTGTACCCGATCACCACGCGCGCGCTCAAGGACGACGCCCGGGGCGCAACCGCCCCGGGCGAG
- 841 LeuTyrProIleThrThrArgAlaLeuLysAspAspAlaArgGlyAlaThrAlaProGlyGlu
- 2584 GAAGAGGAGGAGTTTGACGCGGCCAAACTGGAGCAGGCCCGCGAGATGATCAAGTATATGTCG
- 862 GluGluGluGluPheAspAlaAlaLysLeuGluGlnAlaArgGluMetIleLysTyrMetSer
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- 2710 CTGGCGACCCGGCTGACGCAGCTCGCGCTTCGGCGCGAGCGCCGCCGGAGTACCAGCAGCTT
- 904 LeuAlaThrArgLeuThrGlnLeuAlaLeuArgArgArgAlaProProGluTyrGlnGlnLeu
- 2773 CCGATGGCCGACGTCGGGGGGGCATGA
- 925 ProMetAlaAspValGlyGlyAla •••

Figure No. 2 (end)

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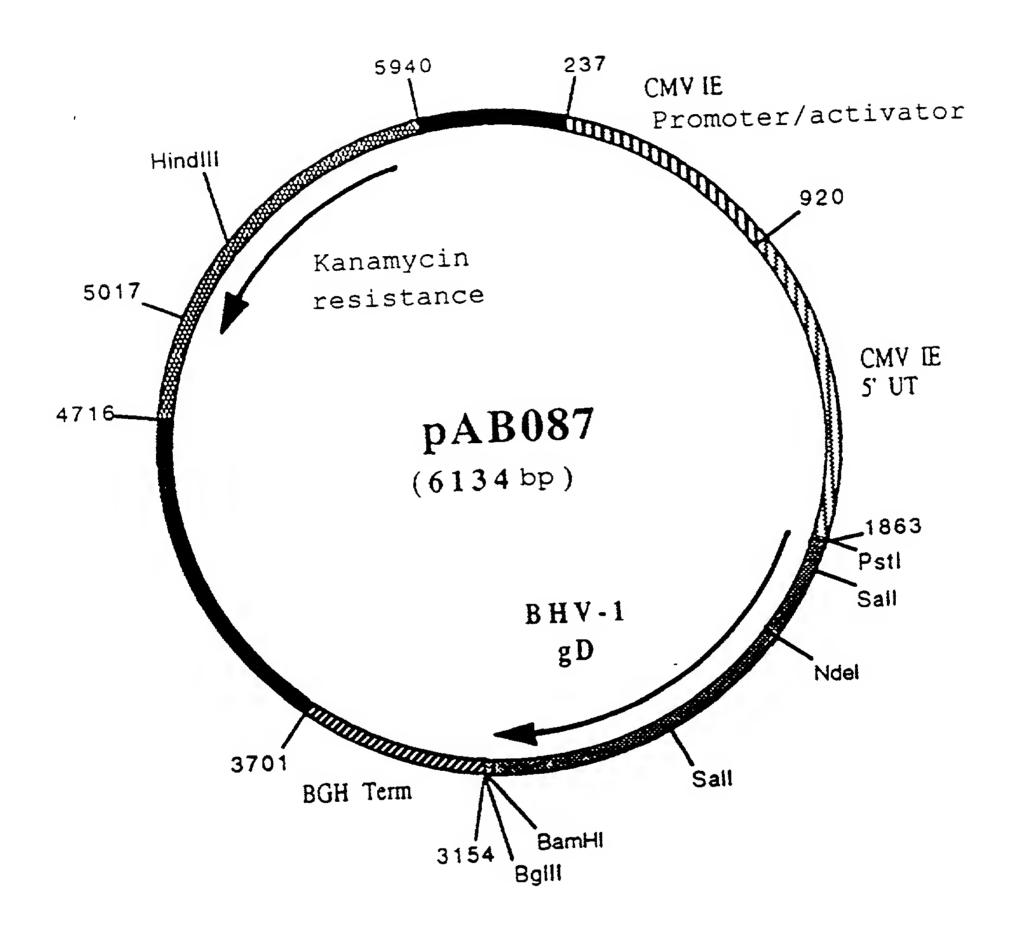


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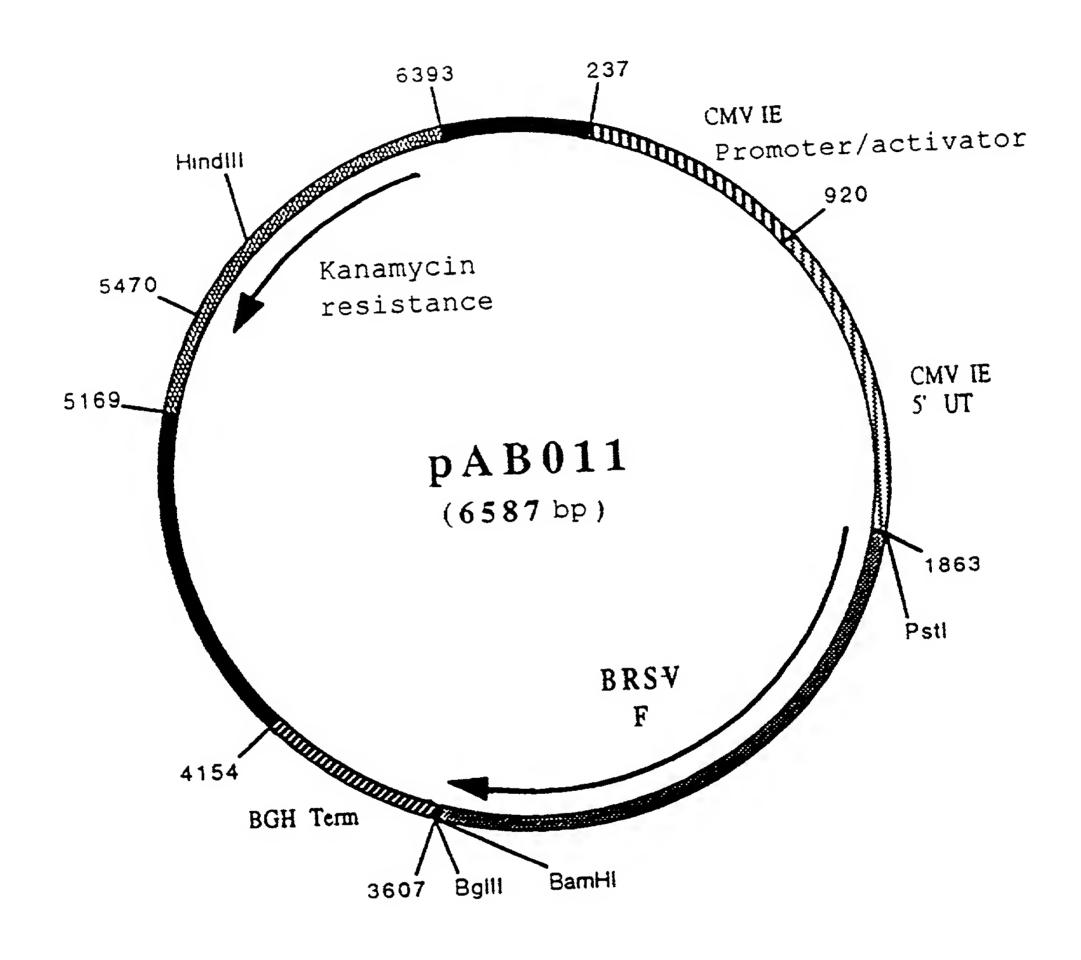


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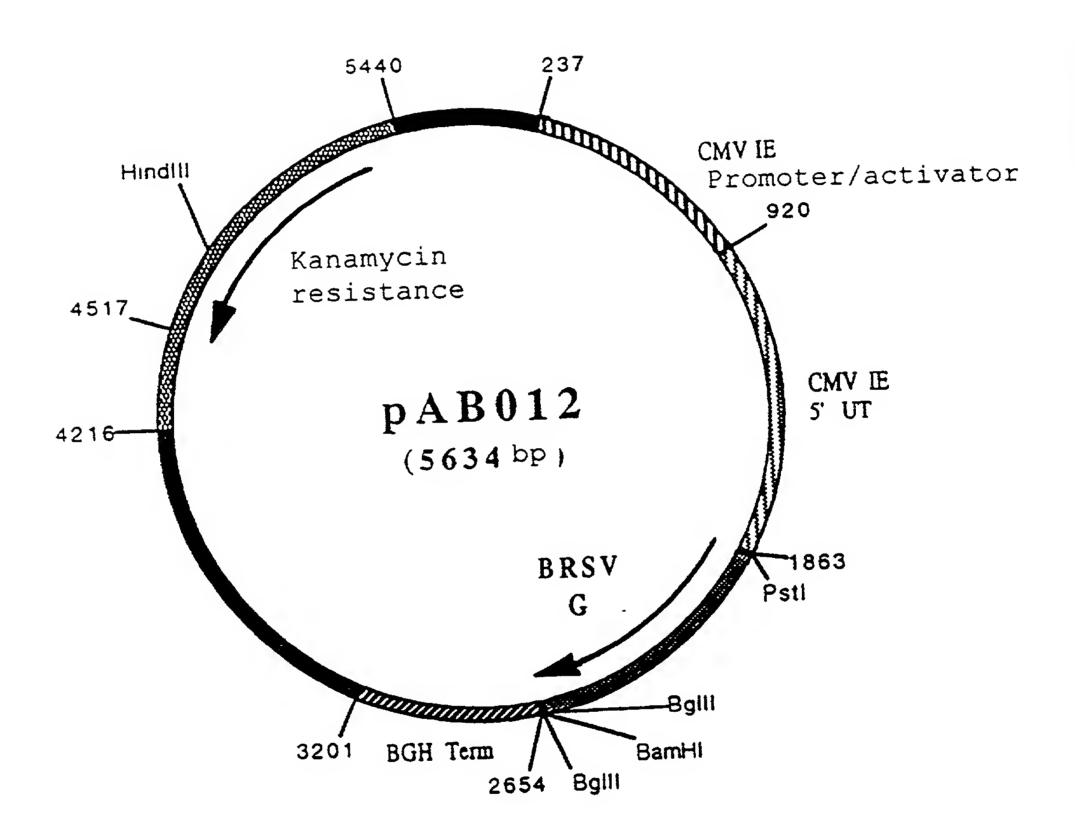


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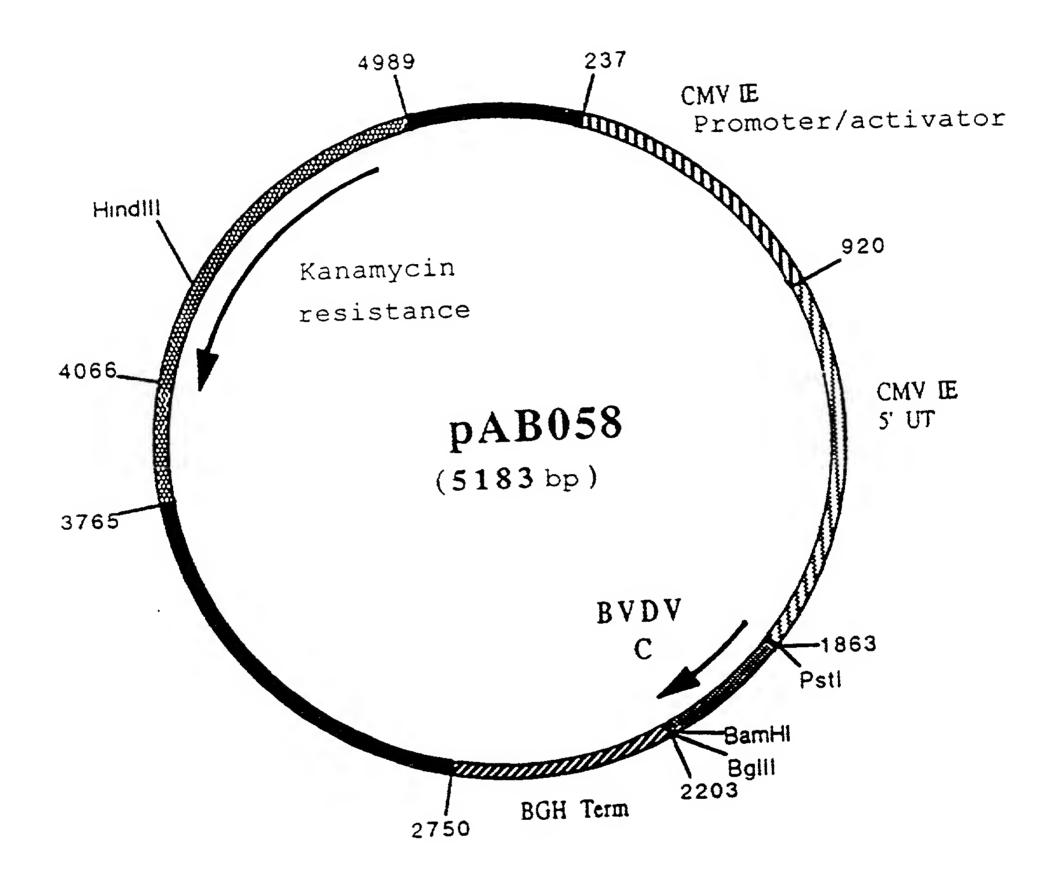


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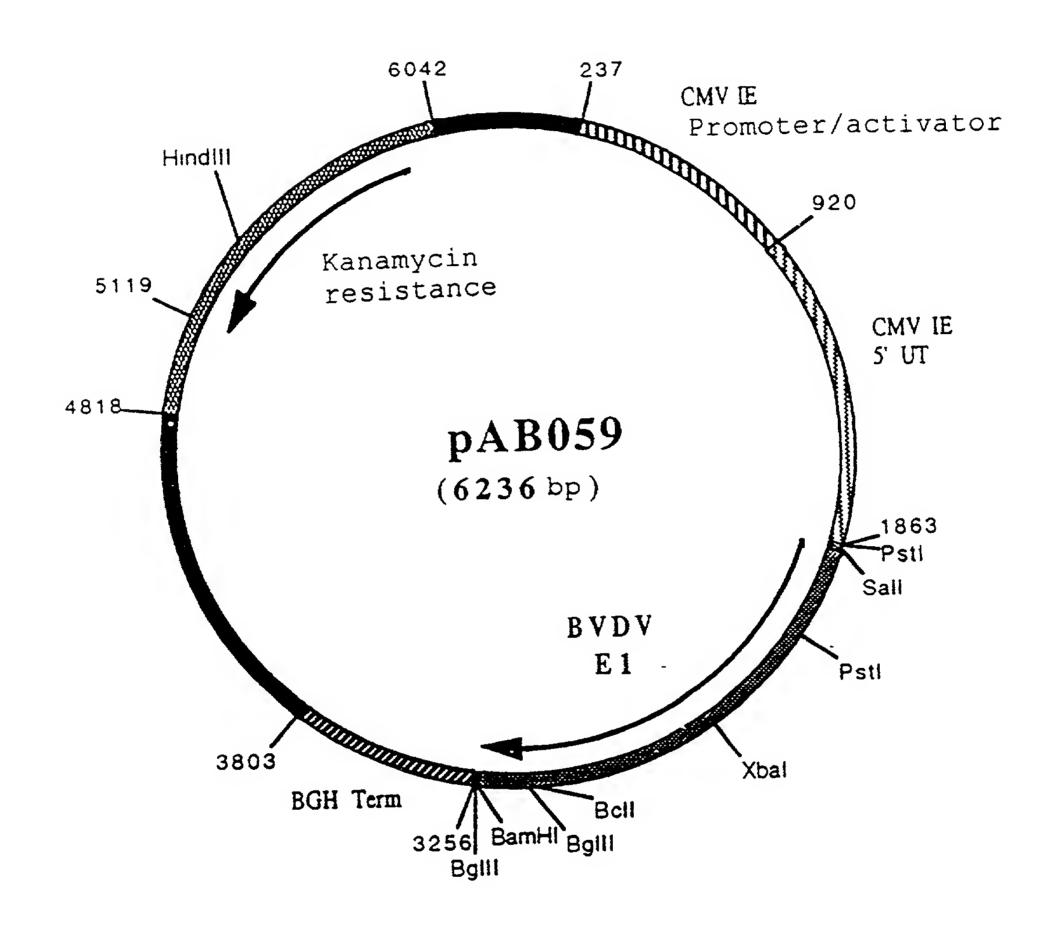


Figure No. 8

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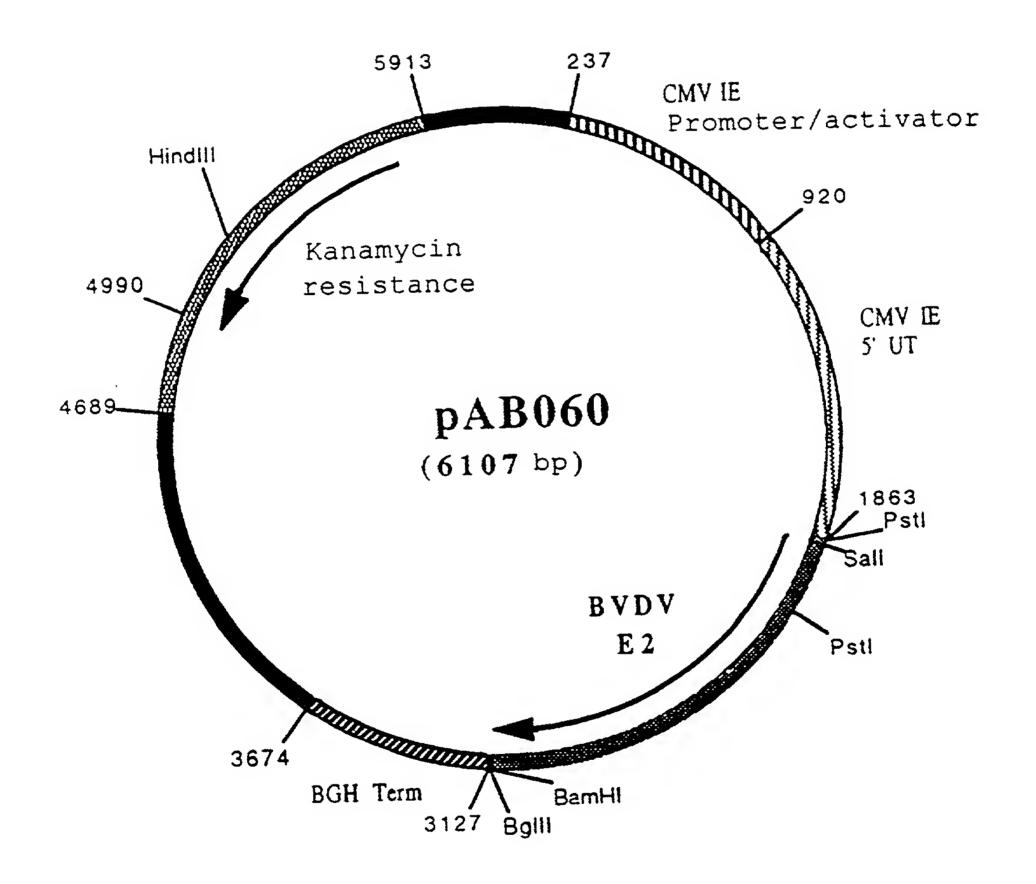


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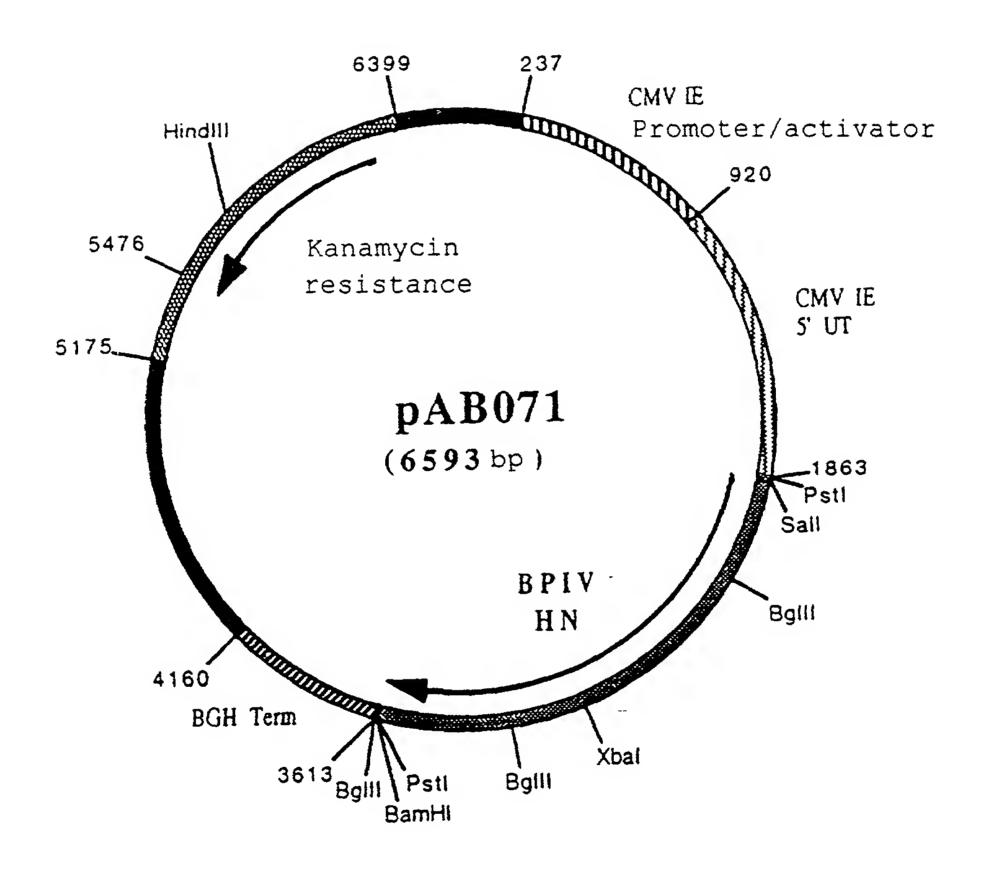


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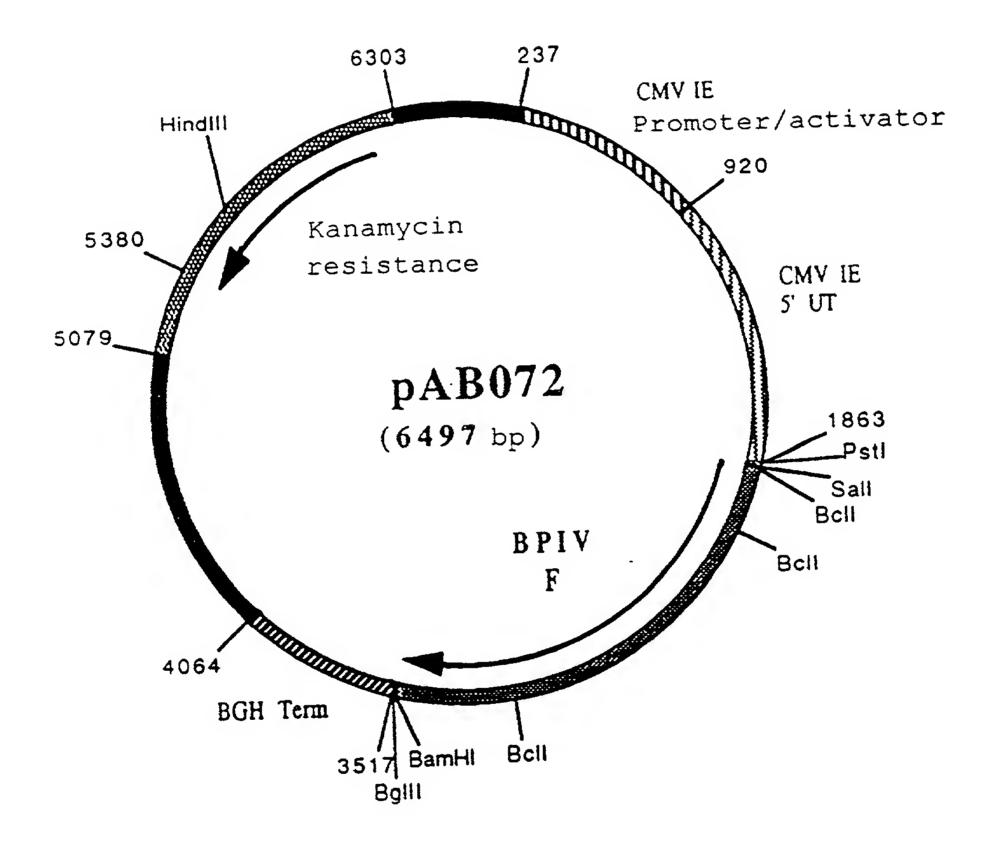


Figure No. 11